



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/954773  
Source: OIPE  
Date Processed by STIC: 10/09/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be downloaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

**Raw Sequence Listing Error Summary**

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/954773</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001  
TIME: 08:45:40

Input Set : A:\2seqlist.app  
Output Set: N:\CRF3\10092001\I954773.raw

3 <110> APPLICANT: Lighfoot, David A.  
4 Gibson, Paul T.  
5 Merkem, Khalid  
7 <120> TITLE OF INVENTION: Soybean Sudden Death Syndrome Resistant Soybeans,  
8 Soybean Cyst Nematode Resistant Soybeans and Methods of  
9 Breeding and Identifying Resistant Plants  
11 <130> FILE REFERENCE: Sou Illinois 1268/2 Sequence Listing  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/954,773  
C--> 14 <141> CURRENT FILING DATE: 2001-09-18  
16 <150> PRIOR APPLICATION NUMBER: 60/035,335  
17 <151> PRIOR FILING DATE: 1997-01-14  
19 <160> NUMBER OF SEQ ID NOS: 20  
21 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

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690 <211> LENGTH: 801  
691 <212> TYPE: DNA  
692 <213> ORGANISM: Glycine max  
694 <400> SEQUENCE: 9  
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696 ttcgtcgacc tcgaggatc acgctaatacg tatattatata atcaactgtc tcaatagatg 120  
697 gcacacaccc tatcttcat aaaattacta cacttttaa tttttgtaat aaaaaaccta 180  
698 gaaaaactca ttatgaaaca gatgatgtac ttttaacact ctgtcggcct ctctctct 240  
699 attatataatt gatttaaatt tattgagaat tatattttt 420  
700 ttatataatt ggatccggc cctctagatg cggccgcatg cataagctt 360  
701 agtgtcacct aaatagctt gctgtatcat ggtcatatgt gtttcctgt tgaaattgtt 420  
E--> 702 atccgctcac aattccacac aacatacggag ccggaagcat aaagtgtt 480  
E--> 703 cctaattgatg gagctaaactc acattaatttgc ctttcgtc actgcccgtc ttccagtcng 540  
E--> 704 gaaacctgtc ctgccagctg cattaatgaa tcngccaacc cncggggana agcngttgc 600  
E--> 705 ntatggcgc tcttncgc tcttcgtca ntgactcgct ggcgtcngtgc nttcngntgc 660  
E--> 706 cgcgaacggt atcancncac tcnaangnng taaatacggt tatccaccna accnngggga 720  
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712 <212> TYPE: DNA  
713 <213> ORGANISM: Glycine max  
715 <400> SEQUENCE: 10  
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717 ccgagctcgat attcgtcgac ctcgaggat cttttatgt tggtagctac tgtaatatacg 120  
718 tcttgtactt ttaacttttta agtctactc ctttggact cttatatacg cttatatacg 180  
719 gtcttgcgtatc tcggacttta atataagcaa atctaactaa ttttgccta ttatataactt 240  
720 tcattcctaa aacacccttc attaattct aattctattt ccaataactc ttttttattc 300  
721 atgataacaa gttccatgtt agacatgtt agaaataacc ttatgttta tttgagatta 360

*Errored  
Must enumerate n's*

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723 atatacgagt ccaaaggag taccaaatgt cacaatgtt ctaaaatgtt ttatatgtt 480  
E--> 724 ctttttaatt catcttgcg ccatanctac ttagctactg tgctctgatc cggccctct 540  
725 agatgcggcc gcatgcataa gcttgagtat ctatagtgtc cctaaatagc ttggcgatc 600  
E--> 726 atggtcatac ctgttccng tggaaattt ttatccgctc acaattccac acaacatacg 660  
E--> 727 anccggaaagc ataaaatgt taagccnngg gtgcataatg agtgagctaa ctcacattaa 720  
E--> 728 ttgcgttgcg ctcactgccc gttccnatt cggaaaactg tcctgnanc tgcattaatg 780  
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734 <213> ORGANISM: Glycine max  
736 <400> SEQUENCE: 11  
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739 agaggggctg attttggaga aaacatcatc catgtataa agtccgttta gattccagct 180  
740 attgttcaca ttcatccctt acatatgaga atatccctat aagctgaaac taactttac 240  
741 aaacaaacat gcacccaacc attaaatgtt gacttaatat ccgggtata atgaccttaa 300  
742 ttcagaaattt cacataaataa actaaaatgtt agtttattt tattttatgtc tggattttact 360  
743 gcacaaacta aacaaaatgtt tggattta gacataaaaa ataccaatgc tggatggaaa 420  
E--> 744 taagaaatgg tggcatata gacaaggttc ttttctgttt tctttaaatt gcagtcnaag 480  
E--> 745 ccatcangag gttcatgtaa ttaaccaaaac tagacgttga cttttgggtt tattcttttg 540  
746 tagaatagca agcaagtcat tataaatctg gccattggaa cagcttagtt taactccgc 600  
E--> 747 cgcaaatttg taaaatattt naataataat atcacctaaa atcatatttg tcanttcatt 660  
E--> 748 ttgttttang ttatataat tatttttt taccttacnt ctttataat ntcaatgtg 720  
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753 <211> LENGTH: 777  
754 <212> TYPE: DNA  
755 <213> ORGANISM: Glycine max  
757 <400> SEQUENCE: 12  
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759 catctagagg gcccggatct ttctgttgc gcaaaattgtt agtctttgc tcattttat 120  
760 caaaattctt aatgaaaatgtt taattacata aaatattttt gtagaaagcaaa ttttacacag 180  
761 ttattttttt aaaaaattac acagtttttca aataacaaat tacaatataat tataaggta 240  
762 taataaaatat tttaaaatccat atataaaaatgtt tgacttatttataatgtt aatgtaaatt 300  
763 ttttacacta ttaaactcat ttacgttgc cttacgttgc acataacttattt ttttcatgtt 360  
764 aatttacaaa aagcttcaa aaataaaaattt attagttgtt ccccccaaaat ataaaatttt 420  
765 tagctatgtt aaaaattttgtt gatatttgcata aaagaaaaaa atattacagt attatattt 480  
766 aaaattttat ttcacacataa aaacacgtt aatgttgcgtt ttgttattt aatgttgc 540  
E--> 767 ctctgtctcg tatttttctc aactctaccg acagcttgc caggttgc ctttcaat 600  
E--> 768 aacaatcgtg gctggaaaca aaaatcgatc tttagaaaga atcngaaatc gtattgacgg 660  
E--> 769 tgcgttttaa aaagactatc caataatctt cttttataa cnctgttgc ctttcaattct 720  
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772 <210> SEQ ID NO: 13  
773 <211> LENGTH: 775  
774 <212> TYPE: DNA  
775 <213> ORGANISM: Glycine max

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777 <400> SEQUENCE: 13  
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E--> 780 taaaattnaa tccatattt antaaaaaaaaaaa aaaaggccna caaattntta aaattcctnc 180  
E--> 781 nncnnttca tantnattt tccttaggtt tttattncaa aantaaaaaaaaaaa ttntattant 240  
E--> 782 tttatnaaaa atagggtnn tgcacnctat tgaaccantn nattaataat atatcttan 300  
E--> 783 ctnatccct caaggtcaac aaanttcana ncncggccna cttggccaat tcnccctata 360  
E--> 784 gtgantcntn ttacaactca ctggccgtcg ttttacaacc tcgtgactgg gaaanccctg 420  
E--> 785 gcgttccca anttaatcnc cttgcaacat ntccccc ttcngctgg gttnataccn 480  
E--> 786 aaaaggcccg cnccgatcgc cttcccnac ttttgcggcc cctnaatggc naatggacgc 540  
E--> 787 ccctgttncg ncncattan ncgcggcg 540  
E--> 788 ttgccagccc cctaaccn ccccttcgc tttctccct cctttctcg ccncttcg 660  
E--> 789 ggnttcccn caagcnctaa atcggggctc cctttagggt tccnaattaa ttgcttacg 720  
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792 <210> SEQ ID NO: 14  
793 <211> LENGTH: 796  
794 <212> TYPE: DNA  
795 <213> ORGANISM: Glycine max  
797 <400> SEQUENCE: 14  
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799 atctagaggg cccggatcag agcacagtag ctaagtagct atgcagcaaa gatgaattaa 120  
800 aaagaagcat ataatacatt ttagtacatt tgtaaaattt ggtactccct ttggactcgt 180  
801 atataagaaa aaataactaa tttcacattna attaagaaag ttagttcaca tcatttaatt 240  
802 ttactaatct caaataaaaaa ataaggttat ttctaaaatg tccttcattt gaaacttggta 300  
803 tcatgaataa aaaagagtta ttggaaatag aattagaatt aaatgaaggg tggtaggaa 360  
804 atgaaaagtat taaataggac aaaatttagt agatttgctt atatttaagt ccgacataca 420  
E--> 805 agaccactct tttgttata tatgagtcca aaggaggat gactaaaaag tttnaaagtnc 480  
806 aagatgatatac tacatgtat accaacataa aaagatccct cgaggtcgac gaattcgagc 540  
807 tcggccgact tggccaaattc ccctatagtg agtcttattt caatttcactg gccgtcg 600  
E--> 808 tacaacgtcn tgactggaa aacctggcg tccccactta tcgccttgca gcacatcccc 660  
E--> 809 ttgcgttccn cccatcccttccca cccatcccttccca acagttgccc 720  
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816 <213> ORGANISM: Glycine max  
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820 ctagagggcc cggatctttt attaaaaattt taatttagtc tcttaattt tgaaaagttt 120  
821 aattaaatca tcaatttata aaaaaatca accatatcct ttattgtttt aaacattata 180  
822 attatgctct ttcaaccaac tctgttagtt taattgtatg aagttttgtt aatagatatt 240  
823 ttacataat ataaataatc ttttacata tattgcagcc aatgtaaaat attatctttt 300  
824 tacattcatt gcttttgatg taaaaattt ttgttttaca tatgttgtt tgacaataaa 360  
825 tataaaaata ttatattttt tcaatttagt taatgtatg atgtgaaaa agatataatt 420  
826 ataataattttt taataatttag agaatttgat tgaactttt aataattaaa aaattaaatg 480  
827 aatttttaat tataattaaa gggatttaattt atatataaa gctttatgtt atttataattt 540  
E--> 828 ttgggtgtcc ncattaatataaaaaggaa tgtaagttaa aaataataat taatattaca 600  
829 taaaacaaaat aaaatgacaa tattattttt tgatattttt attaataattt taaaacaaaattt 660

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001  
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Input Set : A:\2seqlist.app  
Output Set: N:\CRF3\10092001\I954773.raw

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 E--> 846 cggccctgata gacngttttt cggcccttta ctttggagtc cacgttctt aatagtggac 420  
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 E--> 848 ggattttgc gatttcggcc tattggttaa aaaatgagct gatttaacaa aaattnacg 540  
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 E--> 850 atctgtncgg tattttcacc gcatatggt cactctcaat acaatctgt ctgatccnca 660  
 E--> 851 taattttaanc canccccgaa acccgcccaa cacccttaa aacnccccta acgggcttgt 720  
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 E--> 863 ggcgcctgtat gccgcgcatt aagcgcggccg ggtgtgggtt ttcgcncan cgtgaccgct 180  
 864 acacttgccaa ggcgccttagc gcccgcctt ttcgccttccctt tcccttcctt tctcgccacg 240  
 865 ttcgcggct tccccgtca agctctaaat cgggggctcc cttaggggtt ccgatattgt 300  
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 E--> 872 cgcacatattt aaaccaacnc ngaaanccn tccaaannacc cncttaancg ccccaacgg 720  
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 884 ggcgcctccac caccggaca agatacttgg ccattggat tcataaccca tcagcctgtc 180

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885 ccacgtccct tgtgtattct ggactctaaa ctcgacctct catcatctcc gccaaacaaa 240  
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 E--> 888 acngttaccc ggaagatacc cagattgagc ccccacttac taagacnaag cccaacgttn 420  
 E--> 889 cccctcnaga cctgcttctt gaatgactac nanactgact cnangaagaa gctccaacca 480  
 E--> 890 ttngttncen aagttattag ggtngttacc caattagttt agaacgtnt tccgttgaaa 540  
 E--> 891 aggctcatgt taccccccnc ncnntttttt aatnctgaa tanatnatta agaaggcctg 600  
 E--> 892 ccnnagggtta cttactccc tccccnctct ctanatttcc tntangaagc tgccttcccc 660  
 E--> 893 cnaaaattagg ggccattctc ttcccttccc gtctttcac tcccctctgc tcttacnng 720  
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 E--> 895 aanagaagtt ttttcn 796  
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 900 <213> ORGANISM: Glycine max  
 902 <400> SEQUENCE: 19  
 E--> 903 acggcagtga ntgtaatncg actcactata gggcgaattt gccaagtcgg ccgagctcga 60  
 904 attcgtcgcac ctcgagggat cgccgaagta tcgactcaac tattcagaggt agttggcg 120  
 E--> 905 atcgagcgcc atctcgaacc gacgttgctg gccgtacatt tttacngtct cgcngtggat 180  
 E--> 906 ggccggctga agccacacng tggatattgtt ttgctggta cngtgcacgt aaggcttgat 240  
 E--> 907 gaaaacnacgc ggcgagctttt gatccacnat gcccacnacc nagagtagac cagaatctaa 300  
 E--> 908 cacnaatcnc attgtcngat ataacnaaat gcttttaac acgagtgctt cccctnacan 360  
 E--> 909 tggtagattt gagccanctt cccttctcaa tgatacatnc aggatgaacn ntttgacatn 420  
 E--> 910 nctccaccna ttgggnagtc tcatgcacca ccacattccc ncagttatgtt tgaaggtcnt 480  
 E--> 911 tggccngttc ctttananaa atattcctcc gcccnnctag gttgantctc attccnnnaaa 540  
 E--> 912 atatatcccc ttgtccattt ccattcncaa ttctnctgt tngaaagaac ntttgcttcc 600  
 E--> 913 agcnncttc ccaaaacnat tttnngaaa ccctctgtt tcnaagaaat tgggttcanc 660  
 E--> 914 tccaattctn tccatccna aggggttcct ccacttaac cccgnatnan caaccaaggg 720  
 E--> 915 gaattgaaaaa aacggaaag ggaaaaaaat nggcctact tncaaggaa nggcccccc 780  
 E--> 916 tcaagnaaat tthcaagaa gnananaa 808  
 918 <210> SEQ ID NO: 20  
 919 <211> LENGTH: 787  
 920 <212> TYPE: DNA  
 921 <213> ORGANISM: Glycine max  
 923 <400> SEQUENCE: 20  
 E--> 924 ngnncgacgccc ngtgnatgac cactataggg cgaattggcc aagtccggcc agtcgaattt 60  
 925 cgtcgaccc gaggatcta tatataaggct tgcttaagggt agagagagga agactagaga 120  
 E--> 926 ttggatcna caatgcaat aacaaagagt tttaccataat cnaacacaaa tcncattgtc 180  
 E--> 927 ngatataaca aatgctttt taacacgagt gttcacata acagtgttag atttgagccc 240  
 E--> 928 aactccttc tcaatgatac atccnggatg gaccaattt acatgcacca cccnatttggc 300  
 E--> 929 agtctcatgc acaaccacat ttcccacant atgtntgang gtcattggcc ngttcaactaa 360  
 E--> 930 ganaattatt cctcccccagt tcangtngag ttcantccn naaatatagt ccctttgtcc 420  
 E--> 931 natttcnctc tnaaatcctt cctgtggaaa gaccattgca tncagcttc tatcngaaac 480  
 E--> 932 aatattttggaa aaccctctg tttccaaga aatnggtgtc cnctcnatcc tntccctatac 540  
 E--> 933 cnaagggttc atccagttt ccctgattag ancnaagg agtggaaaana ccggggaaagg 600  
 E--> 934 aaaaaatng gccnacttcc aaggaaggcc cttccnctag aaaattttaa gagagagaga 660  
 E--> 935 agatccctt nactttgcc tgcctcnnta tattantcca gtnttatncc cncnanggtg 720  
 E--> 936 gttaccnaan cttttccncc nnaatacngt ctnactaatt tggtaactacc ccncccttn 780  
 E--> 937 gtaccan 787

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/954,773

DATE: 10/09/2001  
TIME: 08:45:41

Input Set : A:\2seqlist.app  
Output Set: N:\CRF3\10092001\I954773.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:695 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9  
M:340 Repeated in SeqNo=9  
L:716 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
M:340 Repeated in SeqNo=10  
L:737 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11  
M:340 Repeated in SeqNo=11  
L:758 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12  
M:340 Repeated in SeqNo=12  
L:778 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13  
M:340 Repeated in SeqNo=13  
L:798 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14  
M:340 Repeated in SeqNo=14  
L:828 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
M:340 Repeated in SeqNo=15  
L:845 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
M:340 Repeated in SeqNo=16

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PATENT APPLICATION: US/09/954,773

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Input Set : A:\2seqlist.app  
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L:861 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17  
M:340 Repeated in SeqNo=17  
L:882 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18  
M:340 Repeated in SeqNo=18  
L:903 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19  
M:340 Repeated in SeqNo=19  
L:924 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
M:340 Repeated in SeqNo=20